-continued

gtaacccgtt gaaccccatt 20

<210> SEQ ID NO 5
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 5

ccatccaatc ggtagtagcg 20

1. An engineered incoherent feed forward loop, comprising:

(i) a first transcription unit comprising a first promoter operably linked to a nucleic acid molecule encoding an endoribonuclease; and

(ii) a second transcription unit comprising a second promoter operably linked to a nucleic acid molecule encoding an output molecule, and an endoribonuclease target site located within the 5' untranslated region (UTR) of the nucleic acid molecule encoding the output molecule,

wherein the endoribonuclease is capable of cleaving the endoribonuclease target site on an RNA transcript expressed by the second transcription unit.

2. The engineered incoherent feed forward loop of claim **1**, wherein the first promoter and the second promoter are identical.

3. The engineered incoherent feed forward loop of claim **2**, wherein the first promoter and the second promoter share the same transcriptional resources.

4. The engineered incoherent feed forward loop of claim **1**, wherein the first promoter and the second promoter are not identical.

5. The engineered incoherent feed forward loop of claim **4**, wherein the first promoter is at least 80% identical to the second promoter.

6. The engineered incoherent feed forward loop of claim **1**, wherein the endoribonuclease is a CRISPR-associated endoribonuclease.

7. The engineered incoherent feed forward loop of claim **6**, wherein the CRISPR-associated endoribonuclease is an endoribonuclease from the Cas6 or Cas13 family optionally wherein the CRISPR-associated endoribonuclease is CasE, Cas6, Csy4, Cse3, PspCas13b, RanCas13b, PguCas13b, or RfxCas13d.

8. (canceled)

9. The engineered incoherent feed forward loop of claim **1**, wherein the first transcription unit further comprises at least one upstream open reading frame (uORF) located within the 5'UTR of the nucleotide sequence encoding the endoribonuclease, optionally wherein the uORF comprises a nucleotide sequence of ACCATGGGTTGA (SEQ ID NO: 1), optionally wherein the first transcription unit comprises 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12 uORFs.

10-11. (canceled)

12. The engineered incoherent feed forward loop of claim **1**, wherein the first transcription unit and the second transcription unit are present on the same nucleic acid or on different nucleic acids.

13. The engineered incoherent feed forward loop of claim **12**, wherein the first transcription unit and the second transcription unit are present on the same vector or on different vectors.

14. The engineered incoherent feed forward loop of claim **1**, wherein the first promoter and/or the second promoter are constitutive promoters, inducible promoters, or tissue specific promoters.

15. A cell comprising the engineered incoherent feed forward loop of claim **1**.

16. A composition comprising the engineered incoherent feed forward loop of claim **1**, or the cell of claim **15**.

17. The composition of claim **16**, further comprising a pharmaceutically acceptable carrier.

18. A method for delivering an output molecule to a subject in need thereof, the method comprising:

delivering to the subject the engineered incoherent feed forward loop of claim **1**.

19. A method for delivering an output molecule to a cell in need thereof, the method comprising:

contacting the cell with the engineered incoherent feed forward loop of claim **1**.

20. A method for maintaining expression level of an output molecule to transcriptional disturbance in a subject in need thereof, the method comprising:

delivering to the subject the engineered incoherent feed forward loop of claim **1**.

21. The method of claim **18**, wherein the first transcription unit and the second transcription unit are delivered on the same nucleic acid or vector.

22. (canceled)

23. The method of claim **18**, wherein the first transcription unit and the second transcription unit are delivered on different nucleic acids or different vectors.

24. (canceled)

25. The method of claim **23**, wherein the ratio between the first transcription unit and the second transcription unit is proportional.

* * * * *